

FIG. 1.

1 GGGAGTCATCATM S D V T I V K E G W V Q K R G E 17
 61 ATATATAAAAACTGGAGGCCAAGATACTTCCTTTTGAAAGACAGATGGCTCATTCATAGG 37
 121 ATATAAAGAGAAAACCTCAAGATGTGGATTTACCTTATCCCTCAACAACCTTTTCAGTGGC 57
 181 AAAATGCCAGTTAATGAAAACAGAACGACCAAGCCAAACACATTTATAATCAGATGTCT 77
 241 CCAGTGGACTACTGTTATAGAGAGAACATTTTCATGTAGATACTCCAGAGGAAAGGGAAGA 97
 301 ATGGACAGAAGCTATCCAGGCTGTAGCAGACAGACTGCAGAGGCAAGAAGAGGAGAGAAT 117
 361 GAATTGTAGTCCAACCTTCACAAATTGATAATATAGGAGAGGAAGAGATGGATGCCTCTAC 137
 421 AACCCATCATAAAAGAAAGACAATGAATGATTTTGACTATTGAAACTACTAGGTAAAGG 157
 481 CACTTTTGGGAAAGTTATTTTGGTTTCGAGAGAAGGCAAGTGAAAATACTATGCTATGAA 177
 541 GATTCTGAAGAAAGAAGTCATTATTGCAAAGGATGAAGTGGCACACACTCTAACTGAAAG 197
 601 CAGAGTATTAAAGAACACTAGACATCCCTTTTTTAACATCCTTGAAATATTCCTTCCAGAC 217
 661 AAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGGCGAGCTGTTTTTCCATT 237
 721 GTCGAGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAATTGTCTC 257
 781 TGCCTTGGACTATCTACATTCCGGAAGATTGTGTACCGTGATCTCAAGTTGGAGAATCT 277
 841 AATGCTGGACAAAGATGGCCACATAAAAATTACAGATTTTGGACTTTGCAAGAAGGGAT 297
 901 CACAGATGCAGCCACCATGAAGACATTCTGTGGCACTCCAGAATATCTGGCACCAGAGGT 317
 961 GTTAGAAGATAATGACTATGGCCGAGCAGTAGACTGGTGGGGCCTAGGGGTTGTCATGTA 337
 1021 TGAAATGATGTGTGGGAGGTACCTTTCTACAACCAGGACCATGAGAACTTTTTGAATT 357
 1081 AATATTAATGGAAGACATTAAATTTCTCAGAACTCTCTTCAGATGCAAAATCATTGCT 377
 1141 TTCAGGGCTCTTGATAAAGGATCCAAATAAACGCCCTTGGTGGAGGACCAGATGATGCAAA 397
 1201 AGAAATTATGAGACACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGATAAAAA 417
 1261 GCTTGTACCTCCTTTTAACTCTCAAGTAACATCTGAGACAGATACTAGATATTTTGATGA 437
 1321 AGAATTTACAGCTCAGACTATTACAATAACACCACCTGAAAAATATGATGAGGATGGTAT 457
 1381 GGACTGCATGGACAATGAGAAGCGCGCCGCTTTCCCTCAATTTTCTACTCTGCAAGTGG 477
 1441 ACGAGAATAAGTCTCTTTCAATTCTGCTACTTCACTGTCACTCTTCAATTTATTACTGAAAA 479
 1501 TGATTCTCTGGACATCACCAGTCCTAGCTCTTACACATAGCAGGGGCA

FIG. 2.

Akt-1 : MGVVAKKEGWAIRGEYIKWRRPRVELIKNDGTFIGYKEPDDVDREAPLNHFSVAQCQLMKTERPPNTEHRCLOWITVIERTFHV : 90
 Akt-2 : MGVSVIKEGWAIRGEYIKWRRPRVELIKSDGTFIGYKEPDDVDREAPLNHFSVAQCQLMKTERPPNTEHRCLOWITVIERTFHV : 90
 Akt-3 : MGVVTKEGVQKRGYIKWRRPRVELIKNDGTFIGYKEPDDVDLP-YPLNHFSVAKCQLMKTERPPNTEHRCLOWITVIERTFHV : 89

Akt-1 : EEPEREERWTAIQVAGLKKQZ--EPPNFRSISDISEAEEEMBSLAKPQHRVITMNEFEYVLKLLGKGTGKVLIVKEKAGHYVAM : 178
 Akt-2 : DSPDEREERWTAIQVANSIQRAPGDDPKYKCSISDSEITTEEMAVASAKAKYIMNDFYLLKLLGKGTGKVLIVKEKAGHYVAM : 180
 Akt-3 : DTPEREERWTAIQVAGLQLOQZ--EPPNCSPTSQIDNIEEEDDASGTHHAKKTMNFEYVLKLLGKGTGKVLIVKEKAGHYVAM : 176

Akt-1 : KILKEVIVAKDEVANTITEERVLKNSRHPFLTILKYSFQIDRLCFVMEYVNGGELFFHLSRERVEEEDRPREYGAEIVSALYLLHSEK : 268
 Akt-2 : KILKEVIVAKDEVANTITEERVLKNSRHPFLTILKYSFQIDRLCFVMEYVNGGELFFHLSRERVEEEDRPREYGAEIVSALYLLHS-R : 269
 Akt-3 : KILKEVIVAKDEVANTITEERVLKNSRHPFLTILKYSFQIDRLCFVMEYVNGGELFFHLSRERVEEEDRPREYGAEIVSALYLLHS-G : 265

Akt-1 : HGVYRDVKLENMLDKDGHKIKITDFGLCKEGIKDPAIMKTCFCTPEYLAPVLELDNDYGRAVDWNGLGVMVYEMCGRLPFYHQDHEKLF : 358
 Akt-2 : DGVYRDVKLENMLDKDGHKIKITDFGLCKEGISDPAIMKTCFCTPEYLAPVLELDNDYGRAVDWNGLGVMVYEMCGRLPFYHQDHERLF : 359
 Akt-3 : KGVYRDVKLENMLDKDGHKIKITDFGLCKEGINDPAIMKTCFCTPEYLAPVLELDNDYGRAVDWNGLGVMVYEMCGRLPFYHQDHEKLF : 355

Akt-1 : ELIINEIIFPRTLQDAKSLLSGILLKQDPQRLGGGSEDAKEHQQHFFAGTWOHVEKKLSPPFKPQVTSEHDTRYFDEFTAQHIT : 448
 Akt-2 : ELIINEIIFPRTLQDAKSLLSGILLKQDPQRLGGGSDAKEVMEHFFELSLWQHVVQKKLLPPFKPQVTSEHDTRYFDEFTAQHIT : 449
 Akt-3 : ELIINEDIKPRTLSSDAKSLLSGILLKQDPNKRLLGGGDDAKEHQRJSEFSGHWQVDDKKLVPPFKPQVTSEHDTRYFDEFTAQHIT : 445

Akt-1 : ITPPQDDI--EVOSEERHEPQFSYSASATA : 480
 Akt-2 : ITPPQDDI--IGLELDQHEPQFSYSASIT : 481
 Akt-3 : ITPPEKDEDDGDDQMNARHEPQFSYSAS : 479

FIG. 3.

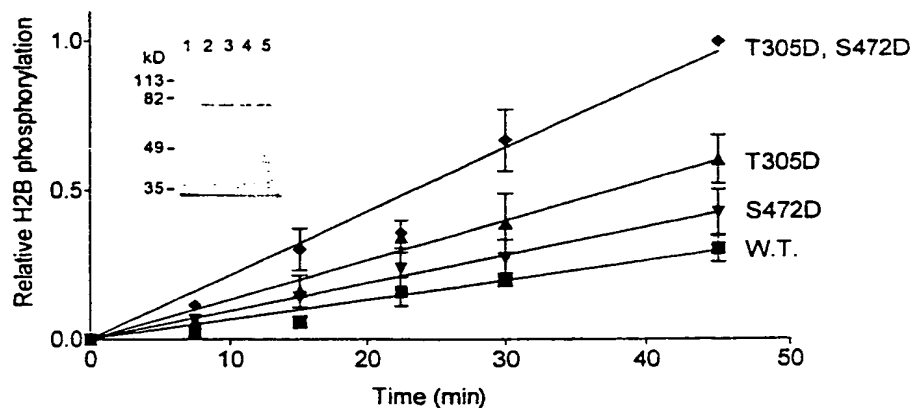
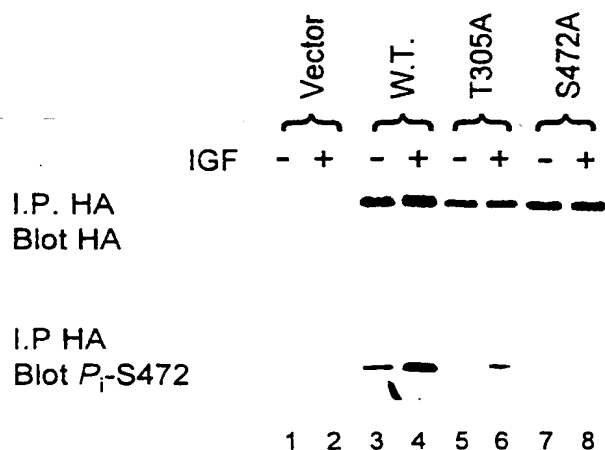
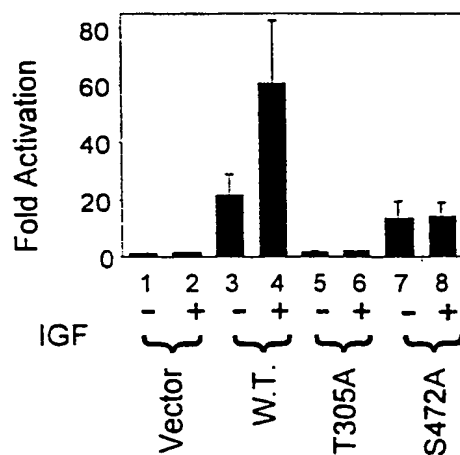
A**B****C**

FIG. 4.

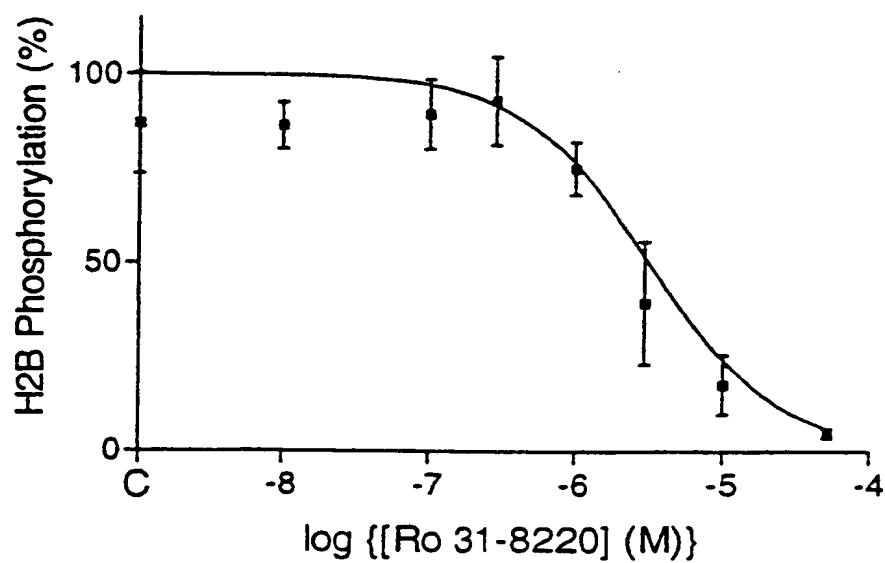
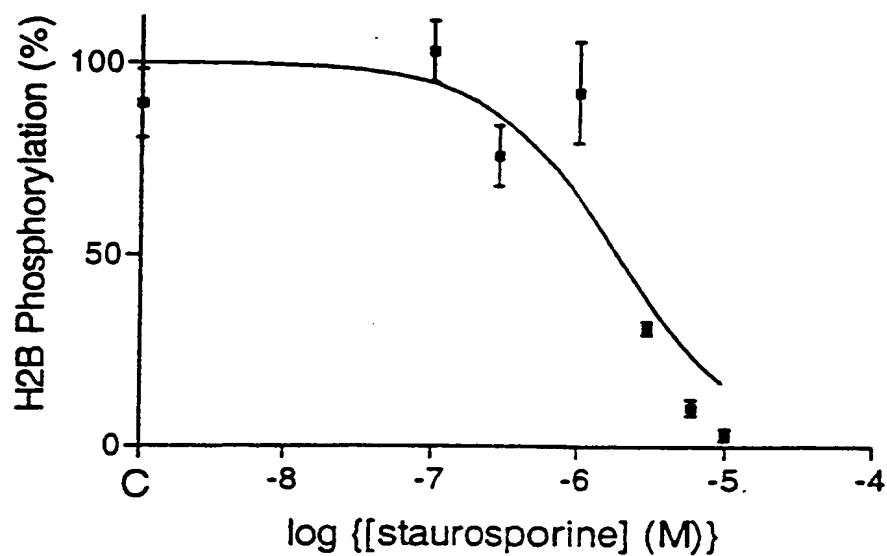


FIG. 5.

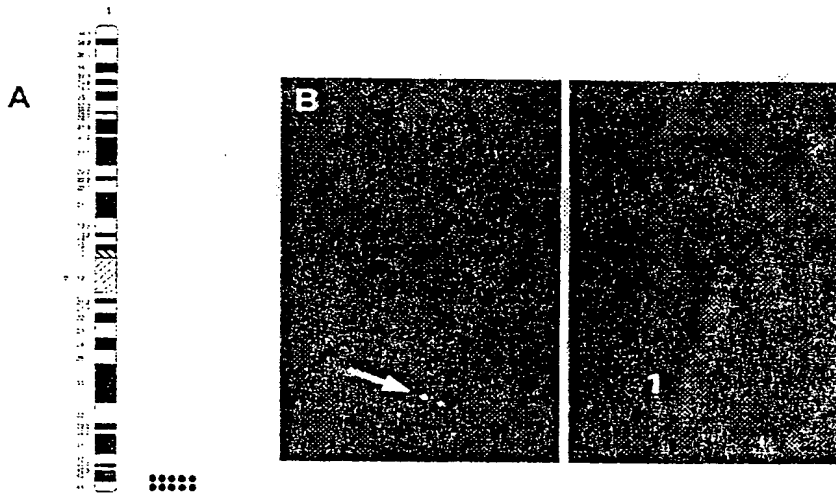


FIG. 6A.

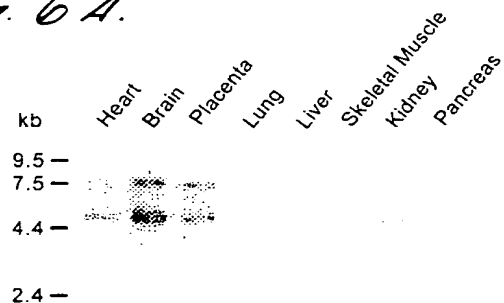


FIG. 6B.

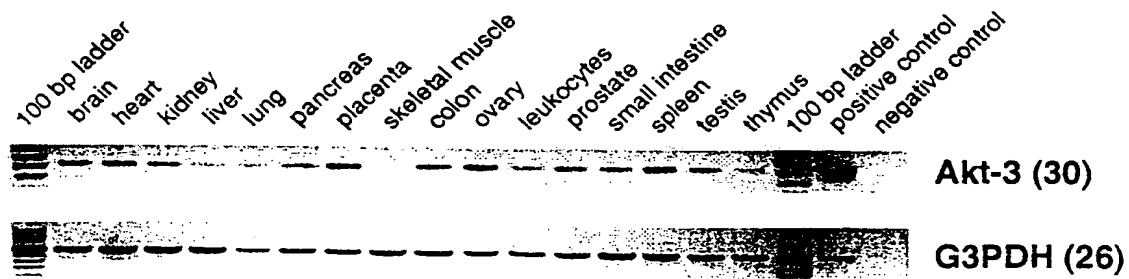


FIG. 6C.

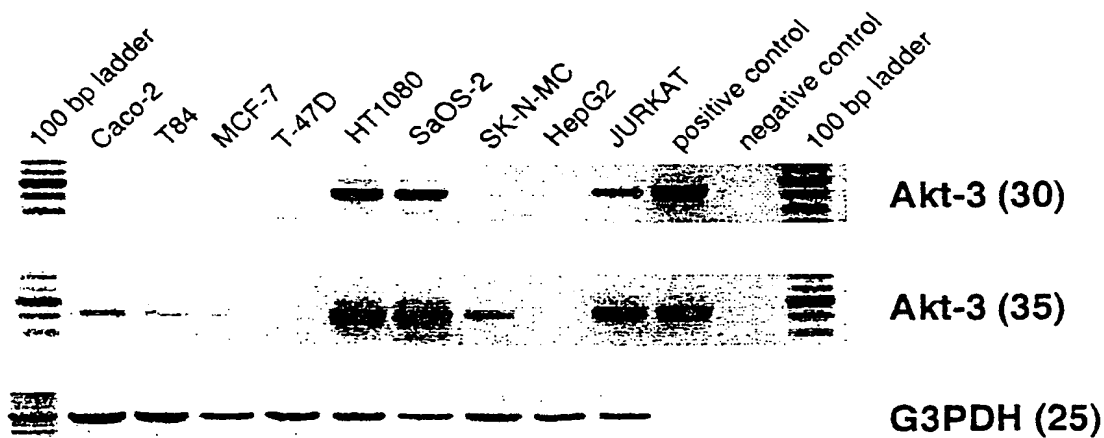


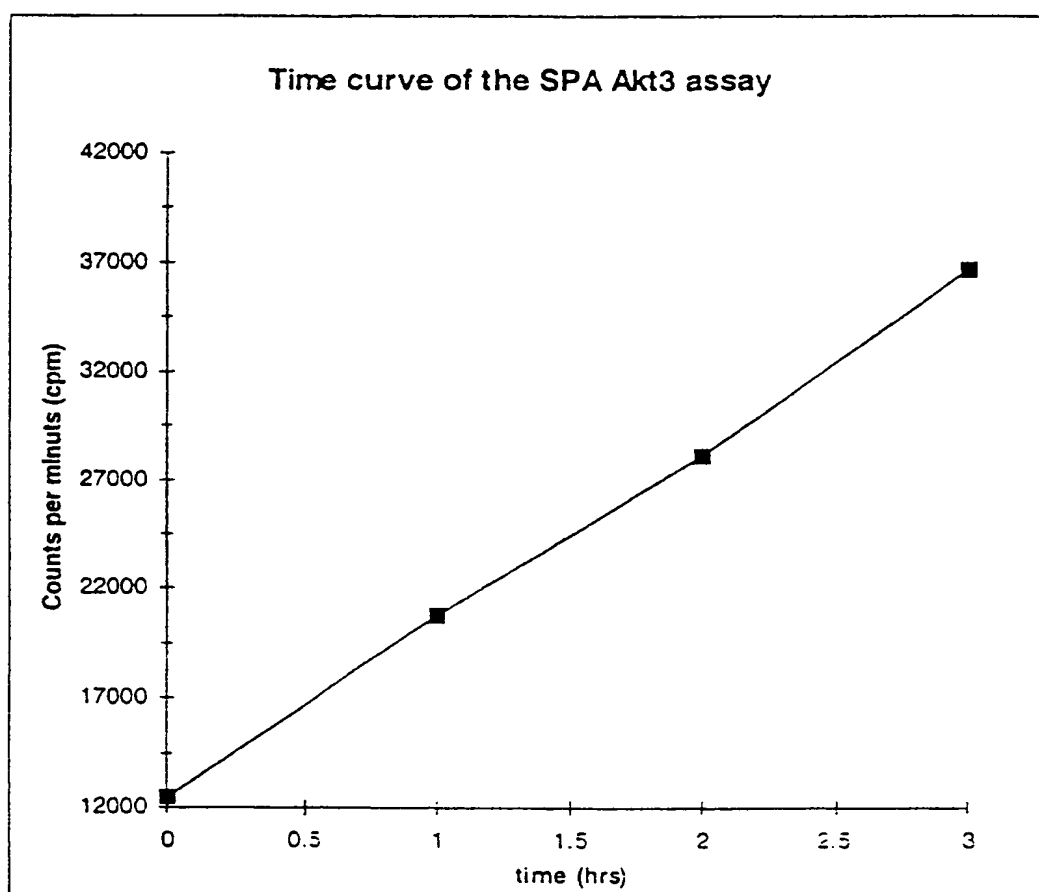
FIG. 7.

FIG. 8.